

SEQUENCE LISTING

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<120> DIAGNOSIS AND TREATMENT OF CARDIOVASCULAR CONDITIONS

<130> P0738/7001/ERP/KA

<150> US 60/227,159  
<151> 2000-08-22

<160> 17

<170> FastSEQ for Windows Version 3.0

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tgagccccgc	ggcgccccgg	gaacttggcg	gcgaccccgag	ccggcgcgagc	cggggcgcgc	300
ctccccccgc	gcgcgcctcc	tgcattgcggg	gccccagactc	cggcgcgcgg	ccggagcccc	360
ccccggccgc	ccccgagccc	cccgcgcccc	gcgcgcgcgc	gcgcgcgcgt	cc atg cac	418
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					1	

cgc ttg atg ggg gtc aac agc acc gcc gcc gcc ggg cag ccc	466
Arg Leu Met Gly Val Asn Ser Thr Ala Ala Ala Ala Gly Gln Pro	
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aat gtc tcc tgc acg tgc aac tgc aaa cgc tct ttg ttc cag agc atg	514
Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln Ser Met	
20 25 30	

gag atc acg gag ctg gag ttt gtt cag atc atc atc atc gtg gtg gtg	562
Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val Val Val	
35 40 45 50	

atg atg gtg atg gtg gtg atc acg tgc ctg ctg agc cac tac aag	610
Met Met Val Met Val Val Ile Thr Cys Leu Leu Ser His Tyr Lys	
55 60 65	

ctg tct gca cggtcc ttc atc agc cggtcac agc cag ggg cggtaggaga	658
Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg Arg Arg	
70 75 80	

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Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser Thr	

85	90	95	
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Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro Arg			
100	105	110	
ccc acc gac cgc ctg gcc gtg ccg ccc ttc gcc cag ccg gag cgc ttc			802
Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg Phe			
115	120	125	130
cac cgc ttc cag ccc acc tat ccg tac ctg cag cac gag atc gac ctg			850
His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp Leu			
135	140	145	
cca ccc acc atc tcg ctg tca gac ggg gag gag ccc cca ccc tac cag			898
Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln			
150	155	160	
ggc ccc tgc acc ctc cag ctt cgg gac ccc gag cag cag ctg gaa ctg			946
Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu			
165	170	175	
aac cgg gag tcg gtg cgc gca ccc cca aac aga acc atc ttc gac agt			994
Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser			
180	185	190	
gac ctg atg gat agt gcc agg ctg ggc ccc tgc ccc ccc agc agt			1042
Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser Ser			
195	200	205	210
aac tcg ggc atc agc gcc acg tgc tac ggc agc ggc ggg cgc atg gag			1090
Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met Glu			
215	220	225	
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Gly Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser			
230	235	240	
tcc ttc cag cac cag agc agt ggg ccg ccc tcc ttg ctg gag ggg			1186
Ser Phe Gln His Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu Gly			
245	250	255	.
acc cgg ctc cac cac aca cac atc gcg ccc cta gag agc gca gcc atc			1234
Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala Ile			
260	265	270	
tgg agc aaa gag aag gat aaa cag aaa gga cac cct ctc tagggcccc			1283
Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu			
275	280	285	
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Gln Pro Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln			

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35	40	45	
Val Val Met Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His			
50	55	60	
Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg			
65	70	75	80
Arg Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu			
85	90	95	
Ser Thr Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro			
100	105	110	
Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu			
115	120	125	
Arg Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile			
130	135	140	
Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro			
145	150	155	160
Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu			
165	170	175	
Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe			
180	185	190	
Asp Ser Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro			
195	200	205	
Ser Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg			
210	215	220	
Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro			
225	230	235	240
Gly Ser Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu			
245	250	255	
Glu Gly Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala			
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Ala Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu			
275	280	285	

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<220>  
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<222> (1)...(861)

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tttgttcaga tcatacatcat cgtgggtgt atgatggta tgggtgtgtt gatcacgtgc	180
ctgctgagcc actacaagct gtctgcacgg tccttcataca gccggcacag ccaggggcgg	240
aggagagaag atgcccgttc ctcagaagga tgcctgtggc cctcggagag cacagtgtca	300
ggcaacggaa tcccagagcc gcagggtctac gccccgcctc ggcccaccga ccgcctggcc	360
gtgccgcctt tcgcccagcg ggagcgcttc caccgcttcc agcccaccta tccgtacctg	420
cagcacgaga tcgacctgtcc acccaccatc tcgctgtcag acggggagga gcccccaccc	480
taccagggcc cctgcaccct ccagcttcgg gaccccgagc agcagcttggaa actgaaccgg	540
gagtcgggtgc ggcacccccc aaacagaacc atcttcgaca gtgacctgtat ggatagtgcc	600
aggctggcg gcccctgccc ccccaagcgt aactcgggca tcagcgccac gtgctacggc	660
agcggcgggc gcatggaggg gccggccccc acctacagcg aggtcatcg ggactaccccg	720
gggtccctt tccagcacca gcagagcgt gggccgcctt cttgtcttggaa ggggacccgg	780
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aaacagaaaag gacaccctct c	861

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Gln Ala Pro Thr Pro Ala Pro Ser Thr Ile Pro Gly Pro Arg Arg Gly	96
15 20 25 30	

tcc ggt cct gag atc ttc acc ttc gac cct ctc ccg gag ccc gca gcg

Ser Gly Pro Glu Ile Phe Thr Phe Asp Pro Leu Pro Glu Pro Ala Ala	144
35 40 45	

gcc cct gcc ggg cgc ccc agc gcc tct cgc ggg cac cga aag cgc agc

Ala Pro Ala Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser	192
50 55 60	

cgc agg gtt ctc tac cct cga gtg gtc cg<sup>g</sup> cag ctg cca gtc gag

Arg Arg Val Leu Tyr Pro Arg Val Val Arg Arg Gln Leu Pro Val Glu	240
65 70 75	

gaa ccg aac cca gcc aaa agg ctt ctc ttt ctg ctg ctc acc atc gtc

Glu Pro Asn Pro Ala Lys Arg Leu Leu Phe Leu Leu Leu Thr Ile Val	288
80 85 90	

ttc tgc cag atc ctg atg gct gaa gag ggt gtg ccg gcg ccc ctg cct

Phe Cys Gln Ile Leu Met Ala Glu Glu Gly Val Pro Ala Pro Leu Pro	336
95 100 105 110	

cca gag gac gcc cct aac gcc gca tcc ctg gc<sup>g</sup> ccc acc cct gtg tcc

Pro Glu Asp Ala Pro Asn Ala Ala Ser Leu Ala Pro Thr Pro Val Ser	384
115 120 125	

ccc gtc ctc gag ccc ttt aat ctg act tcg gag ccc tcg gac tac gct

Pro Val Leu Glu Pro Phe Asn Leu Thr Ser Glu Pro Ser Asp Tyr Ala	432
130 135 140	

ctg gac ctc agc act ttc ctc cag caa cac ccg gcc gcc ttc

Leu Asp Leu Ser Thr Phe Leu Gln Gln His Pro Ala Ala Phe	474
145 150 155	

taa

	477
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<212> PRT  
<213> Homo Sapiens

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35	40	45
Ala Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser Arg Arg		
50	55	60
Val Leu Tyr Pro Arg Val Val Arg Arg Gln Leu Pro Val Glu Glu Pro		
65	70	75
Asn Pro Ala Lys Arg Leu Leu Phe Leu Leu Leu Thr Ile Val Phe Cys		
85	90	95
Gln Ile Leu Met Ala Glu Glu Gly Val Pro Ala Pro Leu Pro Pro Glu		
100	105	110
Asp Ala Pro Asn Ala Ala Ser Leu Ala Pro Thr Pro Val Ser Pro Val		
115	120	125
Leu Glu Pro Phe Asn Leu Thr Ser Glu Pro Ser Asp Tyr Ala Leu Asp		
130	135	140
Leu Ser Thr Phe Leu Gln Gln His Pro Ala Ala Phe		
145	150	155

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<212> DNA  
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ccttaaagtg aaataatttt ttgcaaaggg gtttcctcga tttggagctt tttttttctt	180
ccaccgtcat ttctaactct taaaaccaac tcagttccat c atg gtg atg ttc aag	236
Met Val Met Phe Lys	
1	5

aag atc aag tct ttt gag gtg gtc ttt aac gac cct gaa aag gtg tac	284	
Lys Ile Lys Ser Phe Glu Val Val Phe Asn Asp Pro Glu Lys Val Tyr		
10	15	20

ggc agt ggc gag agg gtg gct ggc cgg gtg ata gtg gag gtg tgt gaa	332	
Gly Ser Gly Glu Arg Val Ala Gly Arg Val Ile Val Glu Val Cys Glu		
25	30	35

gtt act cgt gtc aaa gcc gtt agg atc ctg gct tgc gga gtg gct aaa	380	
Val Thr Arg Val Lys Ala Val Arg Ile Leu Ala Cys Gly Val Ala Lys		
40	45	50

gtg ctt tgg atg cag gga tcc cag cag tgc aaa cag act tcg gag tac	428	
Val Leu Trp Met Gln Gly Ser Gln Gln Cys Lys Gln Thr Ser Glu Tyr		
55	60	65

ctg cgc tat gaa gac acg ctt ctt ctg gaa gac cag cca aca ggt gag	476	
Leu Arg Tyr Glu Asp Thr Leu Leu Glu Asp Gln Pro Thr Gly Glu		
70	75	80

aat gag atg gtg atc atg aga cct gga aac aaa tat gag tac aag ttc	524	
Asn Glu Met Val Ile Met Arg Pro Gly Asn Lys Tyr Glu Tyr Lys Phe		
90	95	100

ggc ttt gag ctt cct cag ggg cct ctg gga aca tcc ttc aaa gga aaa	572
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Gly Phe Glu Leu Pro Gln Gly Pro Leu Gly Thr Ser Phe Lys Gly Lys			
105	110	115	
tat ggg tgt gta gac tac tgg gtg aag gct ttt ctt gac cgc ccg agc			620
Tyr Gly Cys Val Asp Tyr Trp Val Lys Ala Phe Leu Asp Arg Pro Ser			
120	125	130	
cag cca actcaa gag aca aag aaa aac ttt gaa gta gtg gat ctg gtg			668
Gln Pro Thr Gln Glu Thr Lys Lys Asn Phe Glu Val Val Asp Leu Val			
135	140	145	
gat gtc aat acc cct gat tta atg gca cct gtg tct gct aaa aaa gaa			716
Asp Val Asn Thr Pro Asp Leu Met Ala Pro Val Ser Ala Lys Lys Glu			
150	155	160	165
aag aaa gtt tcc tgc atg ttc att cct gat ggg cgg gtg tct gtc tct			764
Lys Lys Val Ser Cys Met Phe Ile Pro Asp Gly Arg Val Ser Val Ser			
170	175	180	
gct cga att gac aga aaa gga ttc tgt gaa ggt gat gag att tcc atc			812
Ala Arg Ile Asp Arg Lys Gly Phe Cys Glu Gly Asp Glu Ile Ser Ile			
185	190	195	
cat gct gac ttt gag aat aca tgt tcc cga att gtg gtc ccc aaa gct			860
His Ala Asp Phe Glu Asn Thr Cys Ser Arg Ile Val Val Pro Lys Ala			
200	205	210	
gcc att gtg gcc cgc cac act tac ctt gcc aat ggc cag acc aag gtg			908
Ala Ile Val Ala Arg His Thr Tyr Leu Ala Asn Gly Gln Thr Lys Val			
215	220	225	
ctg act cag aag ttg tca tca gtc aga ggc aat cat att atc tca ggg			956
Leu Thr Gln Lys Leu Ser Ser Val Arg Gly Asn His Ile Ile Ser Gly			
230	235	240	245
aca tgc gca tca tgg cgt ggc aag agc ctt cgg gtt cag aag atc agg			1004
Thr Cys Ala Ser Trp Arg Gly Lys Ser Leu Arg Val Gln Lys Ile Arg			
250	255	260	
cct tct atc ctg ggc tgc aac atc ctt cga gtt gaa tat tcc tta ctg			1052
Pro Ser Ile Leu Gly Cys Asn Ile Leu Arg Val Glu Tyr Ser Leu Leu			
265	270	275	
atc tat gtt agc gtt cct gga tcc aag aag gtc atc ctt gac ctg ccc			1100
Ile Tyr Val Ser Val Pro Gly Ser Lys Lys Val Ile Leu Asp Leu Pro			
280	285	290	
ctg gta att ggc agc aga tca ggt cta agc agc aga aca tcc agc atg			1148
Leu Val Ile Gly Ser Arg Ser Gly Leu Ser Ser Arg Thr Ser Ser Met			
295	300	305	
gcc agc cga acc agc tct gag atg agt tgg gta gat ctg aac atc cct			1196
Ala Ser Arg Thr Ser Ser Glu Met Ser Trp Val Asp Leu Asn Ile Pro			
310	315	320	325
gat acc cca gaa gct cct ccc tgc tat atg gat gtc att cct gaa gat			1244
Asp Thr Pro Glu Ala Pro Pro Cys Tyr Met Asp Val Ile Pro Glu Asp			
330	335	340	
cac cga ttg gag agc cca aca act cct ctg cta gat gac atg gat ggc			1292
His Arg Leu Glu Ser Pro Thr Pro Leu Leu Asp Asp Met Asp Gly			

345

350

355

tct caa gac agc cct atc ttt atg tat gcc cct gag ttc aag ttc atg Ser Gln Asp Ser Pro Ile Phe Met Tyr Ala Pro Glu Phe Lys Phe Met	1340
360 365 370	
cca cca ccg act tat act gag gtg gat ccc tgc atc ctc aac aac aat Pro Pro Pro Thr Tyr Thr Glu Val Asp Pro Cys Ile Leu Asn Asn Asn	1388
375 380 385	
gtg cag tgagcatgtg gaagaaaaga agcagcttta cctacttgtt tcttttgtc Val Gln	1444
390	
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ccttctgcca tcttaatgt aagctgaaac tggctactg tgctcttagg gttaagccaa	2224
aagacaaaaa aaattttact acttttgaga ttgccccat gtacagaatt atataattct	2284
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<212> PRT

<213> Homo Sapiens

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Val Glu Val Cys Glu Val Thr Arg Val Lys Ala Val Arg Ile Leu Ala 35 40 45
Cys Gly Val Ala Lys Val Leu Trp Met Gln Gly Ser Gln Gln Cys Lys 50 55 60
Gln Thr Ser Glu Tyr Leu Arg Tyr Glu Asp Thr Leu Leu Leu Glu Asp 65 70 75 80
Gln Pro Thr Gly Glu Asn Glu Met Val Ile Met Arg Pro Gly Asn Lys 85 90 95
Tyr Glu Tyr Lys Phe Gly Phe Glu Leu Pro Gln Gly Pro Leu Gly Thr 100 105 110
Ser Phe Lys Gly Lys Tyr Gly Cys Val Asp Tyr Trp Val Lys Ala Phe 115 120 125
Leu Asp Arg Pro Ser Gln Pro Thr Gln Glu Thr Lys Lys Asn Phe Glu 130 135 140
Val Val Asp Leu Val Asp Val Asn Thr Pro Asp Leu Met Ala Pro Val

145                    150                    155                    160  
Ser Ala Lys Lys Glu Lys Lys Val Ser Cys Met Phe Ile Pro Asp Gly  
                      165                    170                    175  
Arg Val Ser Val Ser Ala Arg Ile Asp Arg Lys Gly Phe Cys Glu Gly  
                      180                    185                    190  
Asp Glu Ile Ser Ile His Ala Asp Phe Glu Asn Thr Cys Ser Arg Ile  
                      195                    200                    205  
Val Val Pro Lys Ala Ala Ile Val Ala Arg His Thr Tyr Leu Ala Asn  
                      210                    215                    220  
Gly Gln Thr Lys Val Leu Thr Gln Lys Leu Ser Ser Val Arg Gly Asn  
                      225                    230                    235                    240  
His Ile Ile Ser Gly Thr Cys Ala Ser Trp Arg Gly Lys Ser Leu Arg  
                      245                    250                    255  
Val Gln Lys Ile Arg Pro Ser Ile Leu Gly Cys Asn Ile Leu Arg Val  
                      260                    265                    270  
Glu Tyr Ser Leu Leu Ile Tyr Val Ser Val Pro Gly Ser Lys Lys Val  
                      275                    280                    285  
Ile Leu Asp Leu Pro Leu Val Ile Gly Ser Arg Ser Gly Leu Ser Ser  
                      290                    295                    300  
Arg Thr Ser Ser Met Ala Ser Arg Thr Ser Ser Glu Met Ser Trp Val  
                      305                    310                    315                    320  
Asp Leu Asn Ile Pro Asp Thr Pro Glu Ala Pro Pro Cys Tyr Met Asp  
                      325                    330                    335  
Val Ile Pro Glu Asp His Arg Leu Glu Ser Pro Thr Thr Pro Leu Leu  
                      340                    345                    350  
Asp Asp Met Asp Gly Ser Gln Asp Ser Pro Ile Phe Met Tyr Ala Pro  
                      355                    360                    365  
Glu Phe Lys Phe Met Pro Pro Pro Thr Tyr Thr Glu Val Asp Pro Cys  
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Ile Leu Asn Asn Asn Val Gln  
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<222> (72)...(545)  
<223> BTG2

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Met Ser His Gly Lys Gly Thr Asp Met Leu Pro Glu Ile  
              1                5                10  
                      110

gcc gcc gcc gtg ggc ttc ctc tcc agc ctc ctg agg acc cgg ggc tgc      158  
Ala Ala Ala Val Gly Phe Leu Ser Ser Leu Leu Arg Thr Arg Gly Cys  
              15                20                25

gtg agc gag cag agg ctt aag gtc ttc agc ggg gcg ctc cag gag gca      206  
Val Ser Glu Gln Arg Leu Lys Val Phe Ser Gly Ala Leu Gln Glu Ala  
              30                35                40                45

ctc aca gag cac tac aaa cac cac tgg ttt ccc gaa aag ccg tcc aag      254  
Leu Thr Glu His Tyr Lys His His Trp Phe Pro Glu Lys Pro Ser Lys  
              50                55                60

ggc tcc ggc tac cgc tgc att cgc atc aac cac aag atg gac ccc atc      302



<210> 9  
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1 5 10 15  
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20 25 30  
Gln Arg Leu Lys Val Phe Ser Gly Ala Leu Gln Glu Ala Leu Thr Glu  
35 40 45  
His Tyr Lys His His Trp Phe Pro Glu Lys Pro Ser Lys Gly Ser Gly  
50 55 60  
Tyr Arg Cys Ile Arg Ile Asn His Lys Met Asp Pro Ile Ile Ser Arg  
65 70 75 80  
Val Ala Ser Gln Ile Gly Leu Ser Gln Pro Gln Leu His Gln Leu Leu  
85 90 95  
Pro Ser Glu Leu Thr Leu Trp Val Asp Pro Tyr Glu Val Ser Tyr Arg  
100 105 110  
Ile Gly Glu Asp Gly Ser Ile Cys Val Leu Tyr Glu Glu Ala Pro Leu  
115 120 125  
Ala Ala Ser Cys Gly Leu Leu Thr Cys Lys Asn Gln Val Leu Leu Gly  
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Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu Leu Ser Leu Ser Pro Asp  
1 5 10 15  
  
gtg ccc gtg cca tcc gac cat gga ggg act gag tcc agc cca ggc tgg 155  
Val Pro Val Pro Ser Asp His Gly Gly Thr Glu Ser Ser Pro Gly Trp  
20 25 30  
  
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Gly Ser Ser Gly Pro Trp Ser Leu Ser Pro Ser Asp Ser Ser Pro Ser  
35 40 45  
  
ggg gtc acc tcc cgc ctg cct ggc cgc tcc acc agc cta gtg gag ggc 251  
Gly Val Thr Ser Arg Leu Pro Gly Arg Ser Thr Ser Leu Val Glu Gly  
50 55 60  
  
cgc agc tgt ggc tgg gtg ccc cca ccc cct ggc ttc gca ccg ctg gct 299  
Arg Ser Cys Gly Trp Val Pro Pro Pro Gly Phe Ala Pro Leu Ala  
65 70 75 80  
  
ccc cgc ctg ggc cct gag ctg tca ccc tca ccc act tcg ccc act gca 347  
Pro Arg Leu Gly Pro Glu Leu Ser Pro Ser Pro Thr Ser Pro Thr Ala

85

90

95

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tca gag agt ggg cgc tgc cgc tac ggg gcc aag tgc cag ttt gcc cat Ser Glu Ser Gly Arg Cys Arg Tyr Gly Ala Lys Cys Gln Phe Ala His 115 120 125	443
ggc ctg ggc gag ctg cgc cag gcc aat cgc cac ccc aaa tac aag acg Gly Leu Gly Glu Leu Arg Gln Ala Asn Arg His Pro Lys Tyr Lys Thr 130 135 140	491
gaa ctc tgt cac aag ttc tac ctc cag ggc cgc tgc ccc tac ggc tct Glu Leu Cys His Lys Phe Tyr Leu Gln Gly Arg Cys Pro Tyr Gly Ser 145 150 155 160	539
cgc tgc cac ttc atc cac aac cct agc gaa gac ctg gcg gcc ccg ggc Arg Cys His Phe Ile His Asn Pro Ser Glu Asp Leu Ala Ala Pro Gly 165 170 175	587
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ctt cca ctg tca ccc tct gcc ttc tct gct gcc cct ggc acc ccc ctg Leu Pro Leu Ser Pro Ala Phe Ser Ala Ala Pro Gly Thr Pro Leu 225 230 235 240	779
gct cga aga gac ccc acc cca gtc tgt tgc ccc tcc tgc cga agg gcc Ala Arg Arg Asp Pro Thr Pro Val Cys Cys Pro Ser Cys Arg Arg Ala 245 250 255	827
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cgc atc tct gtt tct gag tgacaaaagt actgccccgt cagatcagct Arg Ile Ser Val Ser Glu 325	1067

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<400> 11

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ccc agc atg gag atc acg gag ctg gag ttc gtg caa atc gtg gtc atc 148  
Pro Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Val Val Ile  
30 35 40

gtg gta gtg atg atg gtg atg gtg gtt atg att acg tgc ctg ctg agc 196  
Val Val Met Met Val Met Val Met Ile Thr Cys Leu Leu Ser  
45 50 55

cac tac aag ctg tca gcc cgc tcc ttc atc agc cga cac agc cag gcc 244  
His Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Ala  
60 65 70 75

agg agg aga gac gat gga ctg tcc tcg gaa gga tgc ctc tgg ccc tca 292  
Arg Arg Arg Asp Asp Gly Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser  
80 85 90

gag agt acg gtg tca ggt gga atg ccg gag cca cag gtc tat gcc ccg 340  
Glu Ser Thr Val Ser Gly Gly Met Pro Glu Pro Gln Val Tyr Ala Pro  
95 100 105

cct cgg ccc act gac cga ctc gct gtg ccc ccc ttc atc cag cgg agc 388  
Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ile Gln Arg Ser  
110 115 120

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125 130 135

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Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly  
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Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn  
160 165 170

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Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp  
175 180 185

ctt ata gac agc acc atg ctg ggg ggc ccc tgt ccc ccc agc agt aac 628

Leu Ile Asp Ser Thr Met Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn		
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Ser Gly Ile Ser Ala Thr Cys Tyr Ser Ser Gly Gly Arg Met Glu Gly		
205	210	215
ccg ccc ccc acc tac agc gag gtc att ggc cac tac cct ggc tcc tcc		724
Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser Ser		
220	225	230
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Phe Gln His Gln Gln Ser Asn Gly Pro Ser Ser Leu Leu Glu Gly Thr		
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cgg ctc cat cac tcg cac att gcc cca ctg gag aac aag gag aag gag		820
Arg Leu His His Ser His Ile Ala Pro Leu Glu Asn Lys Glu Lys Glu		
255	260	265
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Lys Gln Lys Gly His Pro Leu		
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Thr Glu Leu Glu Phe Val Gln Ile Val Val Ile Val Val Val Met Met		
35             40                 45		
Val Met Val Val Met Ile Thr Cys Leu Leu Ser His Tyr Lys Leu Ser		
50             55                 60		
Ala Arg Ser Phe Ile Ser Arg His Ser Gln Ala Arg Arg Arg Asp Asp		
65             70                 75                 80		
Gly Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser Thr Val Ser		
85             90                 95		
Gly Gly Met Pro Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro Thr Asp		
100           105                 110		
Arg Leu Ala Val Pro Pro Phe Ile Gln Arg Ser Arg Phe Gln Pro Thr		
115           120                 125		
Tyr Pro Tyr Leu Gln His Glu Ile Ala Leu Pro Pro Thr Ile Ser Leu		
130           135                 140		
Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly Pro Cys Thr Leu Gln		
145           150                 155                 160		
Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn Arg Glu Ser Val Arg		
165           170                 175		
Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp Leu Ile Asp Ser Thr		
180           185                 190		
Met Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala		
195           200                 205		
Thr Cys Tyr Ser Ser Gly Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr		
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Ser Glu Val Ile Gly His Tyr Pro Gly Ser Ser Phe Gln His Gln Gln		
225           230                 235                 240		

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Pro Leu

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<400> 15

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<212> DNA  
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<223> c or t/u

<221> unsure  
<222> (6837)...(6837)  
<223> a or c

<400> 16

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